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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/023,650

DATE: 01/16/2002

TIME: 18:34:07

TECH CENTER 1600/2900

Input Set : A:\PF135D2.ST25.txt

Output Set: N:\CRF3\01162002\J023650.raw

ENTERED

3 <110> APPLICANT: Moore et al.  
 5 <120> TITLE OF INVENTION: Human Transcription Factor IIA  
 7 <130> FILE REFERENCE: PF135D2  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/023,650  
 C--> 9 <141> CURRENT FILING DATE: 2001-12-21  
 9 <150> PRIOR APPLICATION NUMBER: PCT/US94/10644  
 10 <151> PRIOR FILING DATE: 1994-09-20  
 12 <150> PRIOR APPLICATION NUMBER: US 08/411,635  
 13 <151> PRIOR FILING DATE: 1995-04-11  
 15 <150> PRIOR APPLICATION NUMBER: US 08/845,011  
 16 <151> PRIOR FILING DATE: 1997-04-22  
 18 <160> NUMBER OF SEQ ID NOS: 5  
 20 <170> SOFTWARE: PatentIn version 3.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 804  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapiens  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (190)..(519)  
 30 <223> OTHER INFORMATION:  
 33 <400> SEQUENCE: 1  
 34 ggccccctct agaactagt gatcccccg gctgcagga attcggcacg agctggagag 60  
 36 gtggtcggag aagtaggaac ctctgcggg gctcgtggcg gcttctgtcc gctccgcgga 120  
 38 gggaagcgcc ttccccacag gacatcaatg caagcttgaa taagaaaaac aaattcttcc 180  
 40 tcctaagcc atg gca tat cag tta tac aga aat act act ttg gga aac agt 231  
 41 Met Ala Tyr Gln Leu Tyr Arg Asn Thr Thr Leu Gly Asn Ser  
 42 1 5 10  
 44 ctt cag gag agc cta gat gag ctc ata cag tct caa cag atc acc ccc 279  
 45 Leu Gln Glu Ser Leu Asp Glu Leu Ile Gln Ser Gln Gln Ile Thr Pro  
 46 15 20 25 30  
 48 caa ctt gcc ctt caa gtt cta ctt cag ttt gat aag gct ata aat gca 327  
 49 Gln Leu Ala Leu Gln Val Leu Leu Gln Phe Asp Lys Ala Ile Asn Ala  
 50 35 40 45  
 52 gca ctg gct cag agg gtc agg aac aga gtc aat ttc agg ggc tct cta 375  
 53 Ala Leu Ala Gln Arg Val Arg Asn Arg Val Asn Phe Arg Gly Ser Leu  
 54 50 55 60  
 56 aat acg tac aga ttc tgc gat aat gtg tgg act ttt gta ctg aat gat 423  
 57 Asn Thr Tyr Arg Phe Cys Asp Asn Val Trp Thr Phe Val Leu Asn Asp  
 58 65 70 75  
 60 gtt gaa ttc aga gag gtg aca gaa ctt att aaa gtg gat aaa gtg aaa 471  
 61 Val Glu Phe Arg Glu Val Thr Glu Leu Ile Lys Val Asp Lys Val Lys  
 62 80 85 90  
 64 att gta gcc tgt gat ggt aaa aat act ggc tcc aat act aca gaa tga 519  
 65 Ile Val Ala Cys Asp Gly Lys Asn Thr Gly Ser Asn Thr Thr Glu  
 66 95 100 105  
 68 atagaaaaaa tatgactttt ttacaccatc ttctgttatt cattgctttt gaagagaagc 579

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70 atagaagaga ctttttattt attctagaat tgcagaaatg actacactgt gctaraccag      639
72 agaattccag tagaaagaaa cttgtaactc tgtagcctct tacatcacct ttattataca      699
74 gcatgaaaaa ccataacttt tttttaagga caaaagttgt tgccttccta agaaccttct      759
76 ttaataaact cattttaaaa ctctgaaaaa aaaaaaaaaa aaaaa      804

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79 &lt;210&gt; SEQ ID NO: 2

80 &lt;211&gt; LENGTH: 109

81 &lt;212&gt; TYPE: PRT

82 &lt;213&gt; ORGANISM: Homo sapiens

84 &lt;400&gt; SEQUENCE: 2

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86 Met Ala Tyr Gln Leu Tyr Arg Asn Thr Thr Leu Gly Asn Ser Leu Gln
87 1          5          10          15
90 Glu Ser Leu Asp Glu Leu Ile Gln Ser Gln Gln Ile Thr Pro Gln Leu
91          20          25          30
94 Ala Leu Gln Val Leu Leu Gln Phe Asp Lys Ala Ile Asn Ala Ala Leu
95          35          40          45
98 Ala Gln Arg Val Arg Asn Arg Val Asn Phe Arg Gly Ser Leu Asn Thr
99          50          55          60
102 Tyr Arg Phe Cys Asp Asn Val Trp Thr Phe Val Leu Asn Asp Val Glu
103 65          70          75          80
106 Phe Arg Glu Val Thr Glu Leu Ile Lys Val Asp Lys Val Lys Ile Val
107          85          90          95
110 Ala Cys Asp Gly Lys Asn Thr Gly Ser Asn Thr Thr Glu
111          100          105

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114 &lt;210&gt; SEQ ID NO: 3

115 &lt;211&gt; LENGTH: 29

116 &lt;212&gt; TYPE: DNA

117 &lt;213&gt; ORGANISM: Artificial sequence

119 &lt;220&gt; FEATURE:

120 &lt;223&gt; OTHER INFORMATION: Contains a Bam HI restriction enzyme site

122 &lt;400&gt; SEQUENCE: 3

123 gcggcggatc catggcatat caggtatac 29

126 &lt;210&gt; SEQ ID NO: 4

127 &lt;211&gt; LENGTH: 26

128 &lt;212&gt; TYPE: DNA

129 &lt;213&gt; ORGANISM: Artificial sequence

131 &lt;220&gt; FEATURE:

132 &lt;223&gt; OTHER INFORMATION: Contains complementary sequences to a HindIII site

134 &lt;400&gt; SEQUENCE: 4

135 gcggcaagct tattctgtag tattgg 26

138 &lt;210&gt; SEQ ID NO: 5

139 &lt;211&gt; LENGTH: 121

140 &lt;212&gt; TYPE: PRT

141 &lt;213&gt; ORGANISM: Saccharomyces cerevisiae

143 &lt;400&gt; SEQUENCE: 5

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145 Met Ala Val Pro Gly Tyr Tyr Glu Leu Tyr Arg Arg Ser Thr Ile Gly
146 1          5          10          15
149 Asn Ser Leu Val Asp Ala Leu Asp Thr Leu Ile Ser Asp Gly Arg Ile
150          20          25          30
153 Glu Ala Ser Leu Ala Met Arg Val Leu Glu Thr Phe Asp Lys Val Val

```

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154	35	40	45
157	Ala Glu Thr Leu Lys Asp Asn Thr Gln Ser Lys Leu Thr Val Lys Gly		
158	50	55	60
161	Asn Leu Asp Thr Tyr Gly Phe Cys Asp Asp Val Trp Thr Phe Ile Val		
162	65	70	75
165	Lys Asn Cys Gln Val Thr Val Glu Asp Ser His Arg Asp Ala Ser Gln		
166	85	90	95
169	Asn Gly Ser Gly Asp Ser Ser Val Ile Ser Val Asp Lys Leu Arg Ile		
170	100	105	110
173	Val Ala Cys Asn Ser Lys Lys Ser Glu		
174	115	120	

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date